



IFWO

RAW SEQUENCE LISTING

DATE: 08/20/2004

PATENT APPLICATION: US/10/688,221

TIME: 15:06:28

Input Set : A:\B0411631.txt

Output Set: N:\CRF4\08202004\J688221.raw

6 <110> APPLICANT: Ruoho, Arnold E.
8 Sievert, Michael K.
10 Krebs, Mark P.
12 Geiser, Andrew H.
16 <120> TITLE OF INVENTION: BACTERIORHODOPSIN/G PROTEIN-COUPLED RECEPTOR CHIMERAS
21 <130> FILE REFERENCE: 096429-9146
25 <140> CURRENT APPLICATION NUMBER: 10/688,221
27 <141> CURRENT FILING DATE: 2003-10-16
31 <150> PRIOR APPLICATION NUMBER: US 09/389,835
33 <151> PRIOR FILING DATE: 1999-09-03
37 <150> PRIOR APPLICATION NUMBER: 60/098,950
39 <151> PRIOR FILING DATE: 1998-09-03
43 <160> NUMBER OF SEQ ID NOS: 53
47 <170> SOFTWARE: Word 97 (DOS text file)
51 <210> SEQ ID NO: 1
53 <211> LENGTH: 1626
55 <212> TYPE: DNA
57 <213> ORGANISM: Halobacterium salinarium
61 <220> FEATURE:
63 <221> NAME/KEY: CDS
65 <222> LOCATION: (394)..(1182)
69 <400> SEQUENCE: 1
71 ggatccgacg tgaagatggg gctcccgatg ggtgcaaccg tgaagtccgt cacggctgcg 60
75 tcacgacagg agccgaccag cgacacccag aagggtgcgaa cggttgagtg ccgcaacgat 120
79 cacgagtttt tcgtgcgctt cgagtggtaa cacgcgtgca cgcacgcact tcaccgcggg 180
83 tgtttcgacg ccagccggcc gttgaaccag caggcagcgg gcatttcaca gccgctgtgg 240
87 cccacacact cgggtggggtg cgctattttg gtatggtttg gaatccgcgt gtcggctccg 300
91 tgtctgacgg ttcacgcgtc taaattccgt caccagcgta ccatactgat tgggtcgtag 360
95 agttacacac atatcctcgt taggtactgt tgc atg ttg gag tta ttg cca aca 414
97 Met Leu Glu Leu Leu Pro Thr
99 1 5
103 gca gtg gag ggg gta tcg cag gcc cag atc acc gga cgt ccg gag tgg 462
105 Ala Val Glu Gly Val Ser Gln Ala Gln Ile Thr Gly Arg Pro Glu Trp
107 10 15 20
111 atc tgg cta gcg ctc ggt acg gcg cta atg gga ctc ggg acg ctc tat 510
113 Ile Trp Leu Ala Leu Gly Thr Ala Leu Met Gly Leu Gly Thr Leu Tyr
115 25 30 35
119 ttc ctc gtg aaa ggg atg ggc gtc tcg gac cca gat gca aag aaa ttc 558
121 Phe Leu Val Lys Gly Met Gly Val Ser Asp Pro Asp Ala Lys Lys Phe
123 40 45 50 55
127 tac gcc atc acg acg ctc gtc cca gcc atc gcg ttc acg atg tac ctc 606
129 Tyr Ala Ile Thr Thr Leu Val Pro Ala Ile Ala Phe Thr Met Tyr Leu
131 60 65 70

ENTERED

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135 tcg atg ctg ctg ggg tat ggc ctc aca atg gta ccg ttc ggt ggg gag      654
137 Ser Met Leu Leu Gly Tyr Gly Leu Thr Met Val Pro Phe Gly Gly Glu
139              75                      80                      85
143 cag aac ccc atc tac tgg gcg cgg tac gct gac tgg ctg ttc acc acg      702
145 Gln Asn Pro Ile Tyr Trp Ala Arg Tyr Ala Asp Trp Leu Phe Thr Thr
147              90                      95                      100
151 ccg ctg ttg ttg tta gac ctc gcg ttg ctc gtt gac gcg gat cag gga      750
153 Pro Leu Leu Leu Leu Asp Leu Ala Leu Leu Val Asp Ala Asp Gln Gly
155      105                      110                      115
159 acg atc ctt gcg ctc gtc ggt gcc gac ggc atc atg atc ggg acc ggc      798
161 Thr Ile Leu Ala Leu Val Gly Ala Asp Gly Ile Met Ile Gly Thr Gly
163 120                      125                      130                      135
167 ctg gtc ggc gca ctg acg aag gtc tac tcg tac cgc ttc gtg tgg tgg      846
169 Leu Val Gly Ala Leu Thr Lys Val Tyr Ser Tyr Arg Phe Val Trp Trp
171              140                      145                      150
175 gcg atc agc acc gca gcg atg ctg tac atc ctg tac gtg ctg ttc ttc      894
177 Ala Ile Ser Thr Ala Ala Met Leu Tyr Ile Leu Tyr Val Leu Phe Phe
179              155                      160                      165
183 ggg ttc acc tcg aag gcc gaa agc atg cgc ccc gag gtc gca tcc acg      942
185 Gly Phe Thr Ser Lys Ala Glu Ser Met Arg Pro Glu Val Ala Ser Thr
187              170                      175                      180
191 ttc aaa gta ctg cgt aac gtt acc gtt gtg ttg tgg tcc gcg tat ccc      990
193 Phe Lys Val Leu Arg Asn Val Thr Val Val Leu Trp Ser Ala Tyr Pro
195      185                      190                      195
199 gtc gtg tgg ctg atc ggc agc gaa ggt gcg gga atc gtg ccg ctg aac      1038
201 Val Val Trp Leu Ile Gly Ser Glu Gly Ala Gly Ile Val Pro Leu Asn
203 200                      205                      210                      215
207 atc gag acg ctg ctg ttc atg gtg ctt gac gtg agc gcg aag gtc ggc      1086
209 Ile Glu Thr Leu Leu Phe Met Val Leu Asp Val Ser Ala Lys Val Gly
211              220                      225                      230
215 ttc ggg ctc atc ctc ctg cgc agt cgt gcg atc ttc ggc gaa gcc gaa      1134
217 Phe Gly Leu Ile Leu Leu Arg Ser Arg Ala Ile Phe Gly Glu Ala Glu
219              235                      240                      245
223 gcg ccg gag ccg tcc gcc ggc gac ggc gcg gcc gcg acc agc gac tga      1182
225 Ala Pro Glu Pro Ser Ala Gly Asp Gly Ala Ala Ala Thr Ser Asp
227      250                      255                      260
231 tcgcacacgc aggacagccc cacaaccggc gcggcttttc aacgacacac gatgagtcac 1242
235 ccactcggtc ttgtactcgc acgatcgcgc gacgacggcg acgccgacgg cgactttcca 1302
239 gcgtcgctca acaggtctggc tgcgtcgcg ctcgctggtg cggtctcgt cggtgcggcg 1362
243 ggtctgttcg ccgtgcggtt cctgcggtcg ttccgcatga cgttttggga agcgttcacc 1422
247 gttgttggtg tctccagatt cgtctcggcc atcgtggcgg ccctcgcggg ctaccacctc 1482
251 tacaccacgc ccgacgaçta gcagggcccg ctggcgagcc atcactcccg ctgtggcgag 1542
255 gcgacggccg ttctgtaccg ctaccgccgg cccggagtcc gggacatcgg cggggcgatg 1602
259 cgcacgaac ggtcaccggc atcc
265 <210> SEQ ID NO: 2
267 <211> LENGTH: 262
269 <212> TYPE: PRT
271 <213> ORGANISM: Halobacterium salinarium
275 <400> SEQUENCE: 2

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```

277 Met Leu Glu Leu Leu Pro Thr Ala Val Glu Gly Val Ser Gln Ala Gln
279   1           5           10           15
283 Ile Thr Gly Arg Pro Glu Trp Ile Trp Leu Ala Leu Gly Thr Ala Leu
285           20           25           30
289 Met Gly Leu Gly Thr Leu Tyr Phe Leu Val Lys Gly Met Gly Val Ser
291           35           40           45
295 Asp Pro Asp Ala Lys Lys Phe Tyr Ala Ile Thr Thr Leu Val Pro Ala
297           50           55           60
301 Ile Ala Phe Thr Met Tyr Leu Ser Met Leu Leu Gly Tyr Gly Leu Thr
303   65           70           75           80
307 Met Val Pro Phe Gly Gly Glu Gln Asn Pro Ile Tyr Trp Ala Arg Tyr
309           85           90           95
313 Ala Asp Trp Leu Phe Thr Thr Pro Leu Leu Leu Asp Leu Ala Leu
315           100          105          110
319 Leu Val Asp Ala Asp Gln Gly Thr Ile Leu Ala Leu Val Gly Ala Asp
321           115          120          125
325 Gly Ile Met Ile Gly Thr Gly Leu Val Gly Ala Leu Thr Lys Val Tyr
327           130          135          140
331 Ser Tyr Arg Phe Val Trp Trp Ala Ile Ser Thr Ala Ala Met Leu Tyr
333 145           150          155          160
337 Ile Leu Tyr Val Leu Phe Phe Gly Phe Thr Ser Lys Ala Glu Ser Met
339           165          170          175
343 Arg Pro Glu Val Ala Ser Thr Phe Lys Val Leu Arg Asn Val Thr Val
345           180          185          190
349 Val Leu Trp Ser Ala Tyr Pro Val Val Trp Leu Ile Gly Ser Glu Gly
351           195          200          205
355 Ala Gly Ile Val Pro Leu Asn Ile Glu Thr Leu Leu Phe Met Val Leu
357           210          215          220
361 Asp Val Ser Ala Lys Val Gly Phe Gly Leu Ile Leu Leu Arg Ser Arg
363 225           230          235          240
367 Ala Ile Phe Gly Glu Ala Glu Ala Pro Glu Pro Ser Ala Gly Asp Gly
369           245          250          255
373 Ala Ala Ala Thr Ser Asp
375           260
381 <210> SEQ ID NO: 3
383 <211> LENGTH: 20
385 <212> TYPE: DNA
387 <213> ORGANISM: Artificial Sequence
391 <220> FEATURE:
393 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
395     primer
399 <400> SEQUENCE: 3
401 cgcgtatcca gtcgtgtggc                                20
407 <210> SEQ ID NO: 4
409 <211> LENGTH: 20
411 <212> TYPE: DNA
413 <213> ORGANISM: Artificial Sequence
417 <220> FEATURE:
419 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide

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```

421     primer
425 <400> SEQUENCE: 4
427 cctcctgagg agtcgtgcga                                20
433 <210> SEQ ID NO: 5
435 <211> LENGTH: 91
437 <212> TYPE: DNA
439 <213> ORGANISM: Artificial Sequence
443 <220> FEATURE:
445 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
447     primer
451 <400> SEQUENCE: 5
453 atcctgtacg tgctgttctt cgggttcacc gtcaaggagg cggcggcgca gcagcaggag 60
457 tcggcgacga cgcagaaggc ggagaaggag g                                91
463 <210> SEQ ID NO: 6
465 <211> LENGTH: 96
467 <212> TYPE: DNA
469 <213> ORGANISM: Artificial Sequence
473 <220> FEATURE:
475 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
477     primer
481 <400> SEQUENCE: 6
483 cgggatacgc ggaccacaac acaacggtaa cgttacgcag tactttgaac gtggatgcga 60
487 cctccatgcg cgtgacctcc ttctccgcct tctgcy                                96
493 <210> SEQ ID NO: 7
495 <211> LENGTH: 26
497 <212> TYPE: DNA
499 <213> ORGANISM: Artificial Sequence
503 <220> FEATURE:
505 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
507     primer
511 <400> SEQUENCE: 7
513 gtacatcctg tacgtgctgt tcttcg                                26
519 <210> SEQ ID NO: 8
521 <211> LENGTH: 19
523 <212> TYPE: DNA
525 <213> ORGANISM: Artificial Sequence
529 <220> FEATURE:
531 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
533     primer
537 <400> SEQUENCE: 8
539 acgacgggat acgcggacc                                19
545 <210> SEQ ID NO: 9
547 <211> LENGTH: 22
549 <212> TYPE: DNA
551 <213> ORGANISM: Artificial Sequence
555 <220> FEATURE:
557 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
559     primer
563 <400> SEQUENCE: 9

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565 atcctgtacg tgctgttctt cg 22
571 <210> SEQ ID NO: 10
573 <211> LENGTH: 15
575 <212> TYPE: DNA
577 <213> ORGANISM: Artificial Sequence
581 <220> FEATURE:
583 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
585 primer
589 <400> SEQUENCE: 10
591 cgggatacgc ggacc 15
597 <210> SEQ ID NO: 11
599 <211> LENGTH: 83
601 <212> TYPE: DNA
603 <213> ORGANISM: Artificial Sequence
607 <220> FEATURE:
609 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
611 primer
615 <400> SEQUENCE: 11
617 atcctgtacg tgctgttctt cgggttcacc gcgcgtccc acacgcgcaa gatctccacg 60
621 ctcccgcgcg cgaacatgaa ggg 83
627 <210> SEQ ID NO: 12
629 <211> LENGTH: 75
631 <212> TYPE: DNA
633 <213> ORGANISM: Artificial Sequence
637 <220> FEATURE:
639 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
641 primer
645 <400> SEQUENCE: 12
647 cgggatacgc ggaccacaac acaacggtaa cgttacgcag tactttgaac gtggatgcga 60
651 cgcccttcac gtgcg 75
657 <210> SEQ ID NO: 13
659 <211> LENGTH: 89
661 <212> TYPE: DNA
663 <213> ORGANISM: Artificial Sequence
667 <220> FEATURE:
669 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
671 primer
675 <400> SEQUENCE: 13
677 ggggttcaccg aggtcttcta cctcatccgc aagcagctga caagaaggtc tccgcgtcct 60
681 cgggcgaccc gcagaagtac tacggcaag 89
687 <210> SEQ ID NO: 14
689 <211> LENGTH: 90
691 <212> TYPE: DNA
693 <213> ORGANISM: Artificial Sequence
697 <220> FEATURE:
699 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
701 primer
705 <400> SEQUENCE: 14
707 cacaacggtg acgttacgca gtactttgaa cgtggatgcg acggacttcg cgatcttgag 60
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/688,221DATE: 08/20/2004
TIME: 15:06:29Input Set : A:\B0411631.txt
Output Set: N:\CRF4\08202004\J688221.rawInvalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

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Seq#:1; Line(s) 59,61,63,65,67,69,71,73,75,77,79,81,83,85,87,89,91,93,95,97
Seq#:1; Line(s) 99,101,103,105,107,109,111,113,115,117,119,121,123,125,127
Seq#:1; Line(s) 129,131,133,135,137,139,141,143,145,147,149,151,153,155,157
Seq#:1; Line(s) 159,161,163,165,167,169,171,173,175,177,179,181,183,185,187
Seq#:1; Line(s) 189,191,193,195,197,199,201,203,205,207,209,211,213,215,217
Seq#:1; Line(s) 219,221,223,225,227,229,231,233,235,237,239,241,243,245,247
Seq#:1; Line(s) 249,251,253,255,257,259,261,263,265
Seq#:2; Line(s) 267,269,271,273,275,277,279,281,283,285,287,289,291,293,295
Seq#:2; Line(s) 297,299,301,303,305,307,309,311,313,315,317,319,321,323,325
Seq#:2; Line(s) 327,329,331,333,335,337,339,341,343,345,347,349,351,353,355
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Seq#:4; Line(s) 409,411,413,415,417,419,421,423,425,427,429,431,433
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Seq#:7; Line(s) 495,497,499,501,503,505,507,509,511,513,515,517,519
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Seq#:25; Line(s) 1025,1027,1029,1031,1033,1035,1037,1039,1041,1043,1045
Seq#:25; Line(s) 1047
Seq#:26; Line(s) 1049,1051,1053,1055,1057,1059,1061,1063,1065,1067,1069
Seq#:26; Line(s) 1071,1073,1075,1077,1079,1081
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Seq#:27; Line(s) 1107,1109,1111,1113,1115,1117,1119,1121,1123,1125,1127

VERIFICATION SUMMARY

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